REMARKS

Claims 55-57, 61, 72-74 and 76-81 have been canceled and new claims 82-107 submitted.

Claims 40, 71 and 75 have been amended to require the infectious agent be selected from a specific group of feline viruses. Support for such agents can be found in the specification, for example, on page 12, lines 14-19.

Claims 63-68 have been amended to remove molecules and sequences not relating to feline calicivirus, feline herpesvirus, feline parvovirus or feline leukemia virus.

Claim 70 has been amended to specify the biological specimen is contacted with antigens from several, specific infectious agents. Similarly new claims 98, 106 and 107 state the biological specimen is contacted with antigens from several, specific infectious agents. Support for these claims can be found in the original claims (e.g., claim 23) and in the specification, for example, on page 38, lines 3-4 and on page 40, lines 12-14.

New claims 82-85, 92, 95 and 102 specify the antigen used in the claimed method be at least 85% identical to specific SEQ ID NO's. Support for these claims can be found in the specification, for example, on page 14, lines 16-21, through page 15, lines 1-2.

New claims 86-89, 95 and 104 specify the antigen used in the claimed method be encoded by a nucleic acid molecule at least 85% identical to specific SEQ ID NO's. Support for these claims can be found in the specification, for example, on page 18, lines 5-13.

New claims 92 and 101 specify the antigen used in the claimed method be a particular protein. Support for these claims can be found in the specification, for example, on page 12, lines 9-21, through page 13, lines 1-6.

Accordingly, Applicants submit no new matter has been entered into the application.

I. Restriction Requirement

Applicants have elected to prosecute Group I for further prosecution. Group I, drawn to a method to determine the immune status of an animal, includes claims 40-75. Proteins of Group I claims include SEQ ID NO: 2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, and SEQ ID NO:32. Nucleic acid molecules encoding proteins of Group I claims include SEQ ID NO:1,

SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, and SEQ ID NO:31.

II. Sequence Election

The Examiner has stated that each SEQ ID NO is a unique and separately patentable sequence and therefore, Applicants are required to elect a single SEQ ID NO for prosecution. Applicants have provisionally elected SEQ ID NO:22, with traverse for the following reasons.

The Examiner has stated that inventions (e.g., SEQ ID NO's) are unrelated if it can be shown that they are not disclosed as capable of being used together. Applicants note that the SEQ ID NO's listed in the claims have been disclosed as capable of being used together. Applicants are not claiming the individual proteins represented by the specific SEQ ID NO's. Rather, Applicants are claiming a method of determining the immune status of an animal, the method using one or more proteins represented by the listed SEQ ID NO's. In particular, claims 69, 97 and 106, and 70, 98 and 107 are drawn to methods in which the biological specimen is contacted with antigens from three or four, respectively, separate feline viruses. The choice of viruses, and hence antigens, is based on current vaccine methodology which uses a single vaccine containing immunogens from each of these viruses, and which therefore protects against all of these viruses. Thus, one aspect of Applicants invention is a single test which will determine the need to immunize an animal against infection by any of the viruses to which the currently used multi-immunogen vaccine provides protection. Applicants therefore contend this aspect of the instant invention shows how the separate proteins represented by the disclosed SEQ ID NO's can be used together in a single invention, in a meaningful way.

Furthermore, while the claims do list several SEQ ID NO's, Applicants note that several of the SEQ ID NO's completely overlap with other SEQ ID NO's. For example, SEQ ID NO;4 is a truncated version of SEQ ID NO:2. The following chart illustrates the relationships between the SEQ ID NO's disclosed in the claims:

Feline Calicivirus coat protein

SEQ ID NO:1 SEQ ID NO:2	nFCVCP ₂₀₁₃ PFCVCP ₆₇₁	full-length
SEQ ID NO:3 SEQ ID NO:4	nFCVCP ₁₆₄₁ PFCVCP ₅₄₇	mature

Feline Parvovirus VP2

SEQ ID NO:5 SEQ ID NO:6	nFPVVP2 ₁₇₅₂ PFPVVP2 ₅₈₄	full-length
SEQ ID NO:7 SEQ ID NO:8	nFPVVP2C ₇₂₉ PFPVVP2C ₂₄₃	truncated
SEQ ID NO:11 SEQ ID NO:12	nFPVpVP2 ₁₄₃₁ PFPVpVP2 ₄₇₇	truncated (start at 5' of #5; end at 3' of #7)

Feline Herpesvirus

gB SEQ ID NO:13 SEQ ID NO:14	nFHVgB ₂₈₂₉ PFHVgB ₉₄₃	full-length
SEQ ID NO:15 SEQ ID NO:16	nFHVgB ₇₅₀ PFHVgB ₂₅₀	truncated
gC SEQ ID NO:17 SEQ ID NO:18	nFHVgC ₁₆₀₂ PFHVgC ₅₃₄	full-length
SEQ ID NO:19 SEQ ID NO:20	nFHVgC ₁₄₀₁ PFHVgC ₄₆₇	truncated
SEQ ID NO:21 SEQ ID NO:22	nFHVgC _{1401(opt)} PFHVgC _{467(opt)}	codon-optimized truncated gC
gD SEQ ID NO:23 SEQ ID NO:24 SEQ ID NO:25 SEQ ID NO:26	nFHVgD ₁₁₂₂ PFHVgD ₃₇₄ nFHVgD ₉₀₀ PFHVgD ₃₀₀	full-length truncated

FeLV p27

SEQ ID NO:27 SEQ ID NO:28	nFeLVp27 ₇₈₉ . PFeLVp27 ₂₆₃	mature
SEQ ID NO:29 SEQ ID NO:30	nFeLVgp70 ₁₈₃₀ PFeLVgp70 ₆₁₀	full-length
SEQ ID NO:31 SEQ ID NO:32	nFeLVp27-gp70 ₁₈₃₆ PFeLVp27-gp70 ₆₁₂	Pr65-gag/gp70 fusion

Applicants have included alignments of the protein sequences at the end of this response which clearly illustrate the relationship between overlapping sequences. In view of the overlapping nature of these sequences, Applicants contend that not all of the sequences would need to be searched and therefore no undue burden on the Examiner exists. For example, a search of the prior art for SEQ ID NO:4 would suffice for SEQ ID NO's 1-4. Similarly, a search of the prior art for SEQ ID NO:8 would suffice for SEQ ID NO's 5-12. In fact, Applicants contend the Examiner only need search the prior art for SEQ ID NO's 4, 8, 16, 20, 26, 28 and 30.

In view of the above, Applicants request the Examiner withdraw the sequence election requirement and examine the instantly submitted claim set.

III. Species Election

The Examiner is requiring Applicants to elect one species of recombinant antigen for prosecution stating the species are distinct since their sequences, structures, modes of action, etiologies, etc. are different and therefore each antigen represents a patently distinct subject matter. Applicants have provisionally elected to prosecute a herpesvirus protein, with traverse for the following reasons.

The Examiner is referred to section II of this response. As noted above, one aspect of the present invention is a test capable of determining the immune status of an animal to several different viruses, all of which are protected against by vaccination with a single vaccine. In order to determine the immune status to more than one virus, and consequently to determine the need for the multi-immunogenic vaccine, the claimed method must make use of more than one

antigen (see, for example, claims 69 and 70). Limiting the method to a single antigen makes it useless for determining the need for the commonly used, multi-immunogenic vaccine.

Furthermore, with regard to election of a single species of time, as exemplified by claims 71-74, Applicants note that claims 72-74 have been canceled, obviating this requirement. Therefore, in view of the above, Applicants request the Examiner withdraw the species election requirement and examine the instantly submitted claim set.

CONCLUSION

All of the pending Claims are believed to be in condition for allowance. In the event the Examiner has any questions regarding this Application, the Examiner is invited to contact the undersigned representative at (970) 493-7272, ext. 4174.

Respectfully submitted,

Dated: March 27, 2006

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Alignment of SIN2 & SIN4 from DI-9

	mcstcanvlk	yydwdphfkl	vinpnnflsv	gfcsnplmcc	ypellpefgt
SIN4	• • • • • • • • • •		• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •	
SIN2		iylesilgdd	ewastfdavd	pvvppmhwga	agkifqphpg
SIN4			• • • • • • • • • •	• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
	vlmhhligkv	aagwdpdlpl			
SIN4			ADDGSI	TAPEQGTMVG	GVIAEPSAQM
SIN2	STAADMATGK		SFHTSVNWST		QSLGPLLNPY
SIN4	STAADMATGK	SVDSEWEAFF	SFHTSVNWST	SETQGKILFK	QSLGPLLNPY
SIN2	LEHLAKLYVA	WSGSIEVRFS	ISGSGVFGGK	LAAIVVPPGV	DPVQSTSMLQ
SIN4	LEHLAKLYVA	WSGSIEVRFS	ISGSGVFGGK	LAAIVVPPGV	DPVQSTSMLQ
SIN2	YPHVLFDARQ	VEPVIFCLPD	LRSTLYHLMS		VYNDLINPYA
SIN4	YPHVLFDARQ	VEPVIFCLPD	LRSTLYHLMS	DTDTTSLVIM	VYNDLINPYA
SIN2	NDANSSGCIV	TVETKPGPDF	KFHLLKPPGS	MLTHGSIPSD	LIPKTSSLWI
SIN4	NDANSSGCIV	TVETKPGPDF	KFHLLKPPGS	MLTHGSIPSD	LIPKTSSLWI
SIN2	GNRYWSDITD	FVIRPFVFQA	NRHFDFNQET	AGWSTPRFRP	ISVTITEQNG
SIN4	GNRYWSDITD	FVIRPFVFQA	NRHFDFNQET	AGWSTPRFRP	ISVTITEQNG
SIN2	AKLGIGVATD	YIVPGIPDGW	PDTTIPGELI	PAGDYAITNG	TGNDITTATG
SIN4	AKLGIGVATD	YIVPGIPDGW	PDTTIPGELI	PAGDYAITNG	TGNDITTATG
SIN2	YDTADIIKNN	TNFRGMYICG	SLQRAWGDKK	ISNTAFITTA	TLDGDNNNKI
SIN4	YDTADIIKNN	TNFRGMYICG	SLQRAWGDKK	ISNTAFITTA	TLDGDNNNKI
SIN2	NPCNTIDQSK	IVVFQDNHVG	KKAQTSDDTL		QAIGSDRDRV
SIN4	NPCNTIDQSK	IVVFQDNHVG	KKAQTSDDTL	ALLGYTGIGE	QAIGSDRDRV
SIN2	VRISTLPETG	ARGGNHPIFY	KNSIKLGYVI	RSIDVFNSQI	LHTSRQLSLN
SIN4	VRISTLPETG	ARGGNHPIFY	KNSIKLGYVI	RSIDVFNSQI	LHTSRQLSLN
SIN2	HYLLPPDSFA	VYRIIDSNGS	WFDIGIDSDG	FSFVGVSGFG	KLEFPLSASY
SIN4	HYLLPPDSFA	VYRIIDSNGS	WFDIGIDSDG	FSFVGVSGFG	KLEFPLSASY
SIN2	MGIQLAKIRL	ASNIRSPMTK	L		
SIN4	MGIQLAKIRL	ASNIRSPMTK	L		

Alignment of SING	5, SIN8 and	SIN12 from	DI-9	
SIN6 MSDGAVQPDG	GQPAVRNERA	TGSGNGSGGG	GGGGSGGVGI	STGTFNNQTE
	GQPAVRNERA	TGSGNGSGGG	GGGGSGGVGI	STGTFNNQTE
SIN6 FKFLENGWVE	ITANSSRLVH	LNMPESENYK	RVVVNNMDKT	AVKGNMALDD
	ITANSSRLVH	LNMPESENYK	RVVVNNMDKT	AVKGNMALDD
SIN6 IHVQIVTPWS SIN8	LVDANAWGVW	FNPGDWQLIV	NTMSELHLVS	FEQEIFNVVL
	LVDANAWGVW	FNPGDWQLIV	NTMSELHLVS	FEQEIFNVVL
SIN6 KTVSESATQP SIN8	PTKVYNNDLT	ASLMVALDSN	NTMPFTPAAM	RSETLGFYPW
		ASLMVALDSN		RSETLGFYPW
SIN6 KPTIPTPWRY SIN8	YFQWDRTLIP	SHTGTSGTPT	NVYHGTDPDD GTDPDD	VQFYTIENSV VQFYTIENSV
SIN12 KPTIPTPWRY	YFQWDRTLIP	SHTGTSGTPT	NIYHGTDPDD	VQFYTIENSV
SIN6 PVHLLRTGDE SIN8 PVHLLRTGDE	FATGTFFFDC FATGTFFFDC	KPCRLTHTWQ KPCRLTHTWQ	TNRALGLPPF TNRALGLPPF	LNSLPQSEGA LNSLPQSEGA
SIN12 PVHLLRTGDE	FATGTFFFDC	KPCRLTHTWQ	TNRALGLPPF	LNSLPQSEGA
	DKRRGVTQMG		MRPAEVGYSA	-
	DKRRGVTQMG DKRRGVTQMG	NTDYITEATI NTDYITEATI	MRPAEVGYSA MRPAEVGYSA	PYYSFEASTQ PYYSFEASTQ
SIN6 GPFKTPIAAG			GRQHGQKTTT	TGETPERFTY
SIN8 GPFKTPIAAG SIN12 GPFKIPIAAG		AADGDPRYAF AADGDPRYAF	GRQHGQKTTT GRQHGQKTTT	TGETPERFTY TGETPERFTY
	NO OTTO TEETING		ongnogniii	TODIT DIG II
~	EGDWIQNINF		LPTDPIGGKT	GINYTNIFNT
SIN8 IAHQDTGRYP	EGDWIQNINF	NLPVTNDNVL	LPTDPIGGKT	GINYTNIFNT
SIN12 IAHQDTGRYP	AGDWIQNINF	NLPVTNDNVL	LPTDPIGGKT	GINYTNIFNT
SIN6 YGPLTALNNV	PPVYPNGQIW	DKEFDTDlkp	rlhvnapfvc	qnncpgqlfv
SIN8 YGPLTALNNV	PPVYPNGQIW	DKEFDTD		
SIN12 YGPLTALNNV	PPVYPNGQIW	DKEFDTD		
SIN6 kvapnltney	dpdasanmsr	ivtysdfwwk	gklvfkaklr	ashtwnpiqq
SIN8				
SIN12		• • • • • • • • • •	• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
SIN6 msinvdnqfn	yvpnnigamk	ivyeksqlap	rkly	
_			_	
SIN12				

Alignment of SEQ ID NO's 14 & 16 from DI-9

SIN14 SIN16		RRGSRWQGHS RRGSRWQGHS	- 	SLLGIAATGS SLLGIAATGS	RHGNGSSGLT RHGNGSSGLT
SIN14 SIN16	RLARYVSFIW RLARYVSFIW	IVLFLVGPRP IVLFLVGPRP	VEGQSGSTSE VEGQSGSTSE	QPRRTVATPE QPRRTVATPE	VGVHHQNQLQ VGVHHQNQLQ
SIN14 SIN16		LRASQIEANG LRASQIEANG	PSTFYMCPPP PSTFYMCPPP	SGSTVVRLEP SGSTVVRLEP	PRACPDYKLG PRACPDYKLG
SIN14 SIN16	KNFTEGIAVI KNFTEGIAVI	FKENIAPYKF FKENIAPYKF	KANIYYKNII KANIYYKNII	MTTVWSGSSY MTTVWSGSSY	AVTTNRYTDR AVTTNRYTDR
SIN14 SIN16	~	LIDRRGMCLS LIDRRGMCLS	~	FTAFDRDEDP FTAFDRDEDP	RELPLKPPSS RELPLKPPSS
SIN14 SIN16	tlsrvrgwht		dfhhsgtsvn	civeevdars	vypydsfais
SIN14 SIN16	tgdvihmspf	fglrdgahve	htsyssdrfq	qiegyypidl	dtdytgapvs
SIN14 SIN16	rnfletphvt	vawnwtpksg	rvctlakwre	idemlpmnig	syrftaktis
SIN14 SIN16	atfisntsqf	einrirlgdc	atkeaaeaid	riykskyskt	hiqtgtlety
SIN14 SIN16	larggfliaf	rpmisnelak	lyinelarsn	rtvvdlsall	npsgetvqrt
SIN14 SIN16	rrsvpsnqhh	rsrrstiegg	ietvnnasll	kttssvefam	lqfaydyiqa
	hvnemlsria				_
	davavtqcvn		_		
	qlgennellv				
	lisayvikst				

		nlvimrgman			
SIN14	ssflnnpfga	lavgllilag	ivaaflayry	isrlranpmk	alypvttrnl
		aggdsdpgvd	_	-	
		tshltnmalr		-	

Alignment of SIN18, SIN20 and SIN22 from DI-9

SIN18	mrryrmgrgi	yllyicllyt	ylqfgtsstt	avSIENSDNS	TAEMLSSTSM
SIN20				SIENSDNS	TAEMLSSTSM
SIN22	$m\ldots\ldots$			SIENSDNS	TAEMLSSTSM
SIN18	SATTPISQPT	SPFTTPTRRS	TNIATSSSTT	QASQPTSTLT	
SIN20	SATTPISQPT	SPFTTPTRRS	TNIATSSSTT	QASQPTSTLT	TLTRSSTTIA
SIN22	SATTPISQPT	SPFTTPTRRS	TNIATSSSTT	QASQPTSTLT	TLTRSSTTIA
SIN18	TSPSTTQAAT	FIGSSTDSNT	ייז.ז.אייייאאסא	RKKNKNNGAR	FKLYCGYKGV
SIN20	TSPSTTQAAT	FIGSSTDSNT		RKKNKNNGAR	
SIN20	TSPSTTQAAT	FIGSSTDSNT		RKKNKNNGAR	-
011122	IDIDIIQAAI	TIGOSTOSMI	IDDKIIKKEK	MADIMINIM	FREGCGIRGV
SIN18	IYRPYFSPLQ	LNCTLPTEPH	ITNPIDFEIW	FKPRTRFGDF	LGDKEDFVGN
SIN20	IYRPYFSPLQ	LNCTLPTEPH	ITNPIDFEIW	FKPRTRFGDF	LGDKEDFVGN
SIN22	IYRPYFSPLQ	LNCTLPTEPH	ITNPIDFEIW	FKPRTRFGDF	LGDKEDFVGN
SIN18	HTRTSILLFS	SRNGSVNSMD	LGDATLGILQ	SRIPDYTLYN	IPIQHTEAMS
SIN20	HTRTSILLFS	SRNGSVNSMD	LGDATLGILQ	SRIPDYTLYN	IPIQHTEAMS
SIN22	HTRTSILLFS	SRNGSVNSMD	LGDATLGILQ	SRIPDYTLYN	IPIQHTEAMS
SIN18	LGIKSVESAT	SGVYTWRVYG	${\tt GDVLNKTVLG}$	QVNVSVVAYH	PPSVNLTPRA
SIN20	LGIKSVESAT	SGVYTWRVYG	${\tt GDVLNKTVLG}$	QVNVSVVAYH	PPSVNLTPRA
SIN22	LGIKSVESAT	SGVYTWRVYG	${\tt GDGLNKTVLG}$	QVNVSVVAYH	PPSVNLTPRA
SIN18	SLFNKTFEAV	CAVANYFPPR	STKLTWYLDG	KPIERQYISD	TASVWIDGLI
SIN20	SLFNKTFEAV	CAVANYFPPR	STKLTWYLDG	KPIERQYISD	TASVWIDGLI
SIN22	SLFNKTFEAV	CAVANYFPPR	STKLTWYLDG	KPIERQYISD	TASVWIDGLI
G T111 0			D.C.D.I. T.I. T.I.		
SIN18	TRSSVLAIPT	TETDSEKPDI	RCDLEWHESP	VSYKRFTKSV	
SIN20	TRSSVLAIPT	TETDSEKPDI	RCDLEWHESP		APDVYYPPTV
SIN22	TRSSVLAIPT	TETDSEKPDI	RCDLEWHESP	VSYKRFTKSV	APDVYYPPTV
SIN18	SVTFADTRAI	CDVKCVPRDG	ISLMWKIGNY	HLPKAMSADI	LITGPCIERP
SIN20	SVTFADTRAI	CDVKCVPRDG	ISLMWKIGNY	HLPKAMSADI	LITGPCIERP
SIN22	SVTFADTRAI	CDVKCVPRDG	ISLMWKIGNY		LITGPCIERP
011122	OVIII DIII II	CD VIIC VI INDO	102111111120111		DITOT CIBRE
SIN18	GLVNIQSMCD	ISETDGPVSY	TCQTIGYPPI	LPGFYDTQVY	DASPEIVSEs
SIN20	GLVNIQSMCD	ISETDGPVSY	TCQTIGYPPI	LPGFYDTQVY	DASPEIVSE.
SIN22	GLVNIQSMCD	ISETDGPVSY	TCQTIGYPPI	LPGFYDTQVY	DASPEIVS
SIN18	mlvsvvavil	gavlitvfif	italclyysh	prrl	
SIN20					
SIN22					

Alignment of SEQ ID NO's 24 & 26 from DI-9

2	KKTYNATISW				
CIMIZ	TKYMFLTDDE	T.CT.TMMA DAO	FNOCOVDDVI	TTCCMEVTO	EMMOI COMPC
			="		
SIN26	TKYMFLTDDE	LGLIMMAPAQ	FNQGQYRRVI	TIDGSMFYTD	FMVQLSPTPC
SIN24	WFAKPDRYEE	ILHEWCRNVK	TIGLDGARDY	HYYWVPYNPQ	PHHKAVLLYW
SIN26	WFAKPDRYEE	ILHEWCRNVK	TIGLDGARDY	HYYWVPYNPQ	PHHKAVLLYW
CINIDA	YRTHGREPPV	DECEVIDAD	DATDCCCEDC	KDCMDCDCFC	CCDMUTDIEN
		-			
SIN26	YRTHGREPPV	RFQEAIRYDR	PAIPSGSEDS	KRSNDSRGES	SGPNWIDIEN
	YTPKNNVPII	ISDDDVPTAP	PKGMNNOSVV	ipaivlscli	ialilgviyy
SIN24	YTPKNNVPII			_	
SIN24	YTPKNNVPII YTPKNNVPII			ipaivlscli	
SIN24 SIN26		ISDDDVPTAP	PKGMNNQS	_	
SIN24 SIN26 SIN24	YTPKNNVPII	ISDDDVPTAP ayqqlpiiht	PKGMNNQS	_	